RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10 531 543

Source: PCT

Date Processed by STIC: 4-26-05

ENTERED

PCT

RAW SEQUENCE LISTING   DATE: 04/26/2005
PATENT APPLICATION: US/10/531,543   TIME: 15:48:06

Input Set : A:\PCT-KR2003-002190(Sequence List).txt
Output Set: N:\CRF4\04262005\J531543.raw

```
    1 <110> APPLICANT: SUNGKYUNKWAN UNIVERSITY
    3 <120> TITLE OF INVENTION: Composition for treating virus infection disease comprising
Jab1
C--> 5 <140> CURRENT APPLICATION NUMBER: US/10/531,543
C--> 5 <141> CURRENT FILING DATE: 2005-04-15
W--> 0 <130> FILE REFERENCE:
    5 <160> NUMBER OF SEQ ID NOS: 6
    7 <170> SOFTWARE: KopatentIn 1.71
    9 <210> SEQ ID NO: 1
   10 <211> LENGTH: 1262
   11 <212> TYPE: DNA
   12 <213> ORGANISM: Homo sapiens
   14 <220> FEATURE:
   15 <221> NAME/KEY: gene
   16 <222> LOCATION: (1)..(1262)
   17 <223> OTHER INFORMATION: Jab1
   20 <220> FEATURE:
   21 <221> NAME/KEY: CDS
   22 <222> LOCATION: (94)..(1095)
   24 <400> SEQUENCE: 1
   25 ctggtgggga aggtccaaag cccgcacgct gaggcccagt agaagaaagt tgcatcttga          60
   27 ttgtggagcg acagcttctc cggtgcctcg gcc          atg gca gct tcc ggg         108
   28                                              Met Ala Ala Ser Gly
   29                                              1                 5
   31 agt ggt atg gcc cag aaa acc tgg gaa ttg gcc aac aac atg cag gaa         156
   32 Ser Gly Met Ala Gln Lys Thr Trp Glu Leu Ala Asn Asn Met Gln Glu
   33               10                  15                  20
   35 gcg cag agt atc gat gaa atc tac aaa tat gac aaa aaa caa caa caa         204
   36 Ala Gln Ser Ile Asp Glu Ile Tyr Lys Tyr Asp Lys Lys Gln Gln Gln
   37               25                  30                  35
   39 gaa atc ctg gcg gcg aaa ccc tgg act aag gat cac cac tac ttt aaa         252
   40 Glu Ile Leu Ala Ala Lys Pro Trp Thr Lys Asp His His Tyr Phe Lys
   41               40                  45                  50
   43 tac tgc aaa atc tca gca ttg gct cta ctg aaa atg gtg atg cat gcc         300
   44 Tyr Cys Lys Ile Ser Ala Leu Ala Leu Leu Lys Met Val Met His Ala
   45      55                  60                  65
   47 agg tca gga ggc aac ttg gaa gtg atg ggt ttg atg ctc ggg aaa gtc         348
   48 Arg Ser Gly Gly Asn Leu Glu Val Met Gly Leu Met Leu Gly Lys Val
   49 70                  75                  80                  85
   51 gac ggc gag acc atg atc atc atg gac agt ttc gct ttg cct gta gag         396
   52 Asp Gly Glu Thr Met Ile Ile Met Asp Ser Phe Ala Leu Pro Val Glu
   53               90                  95                  100
   55 ggc aca gaa act cga gta aat gct caa gct gct gcg tat gag tat atg         444
   56 Gly Thr Glu Thr Arg Val Asn Ala Gln Ala Ala Ala Tyr Glu Tyr Met
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57                   105                  110                 . 115
59 gct gca tac ata gaa aat gcc aaa cag gtt ggc cgc ctt gag aat gca        492
60 Ala Ala Tyr Ile Glu Asn Ala Lys Gln Val Gly Arg Leu Glu Asn Ala
61           120                 125                 130
63 atc ggt tgg tat cat agc cac cct ggt tat ggc tgc tgg ctc tcc ggg        540
64 Ile Gly Trp Tyr His Ser His Pro Gly Tyr Gly Cys Trp Leu Ser Gly
65           135                 140                 145
67 att gat gtt agt aca cag atg ctg aac cag cag ttt caa gaa cca ttt        588
68 Ile Asp Val Ser Thr Gln Met Leu Asn Gln Gln Phe Gln Glu Pro Phe
69 150                 155                 160                 165
71 gta gca gtg gtg att gat cca acc aga aca atc tct gca gga aaa gtg        636
72 Val Ala Val Val Ile Asp Pro Thr Arg Thr Ile Ser Ala Gly Lys Val
73                 170                 175                 180
75 aat ctt ggc gcc ttt agg aca tat cca aag ggc tac aaa cct cct gat        684
76 Asn Leu Gly Ala Phe Arg Thr Tyr Pro Lys Gly Tyr Lys Pro Pro Asp
77           185                 190                 195
79 gaa gga cct tct gag tac cag act atc cca ctt aat aaa ata gaa gat        732
80 Glu Gly Pro Ser Glu Tyr Gln Thr Ile Pro Leu Asn Lys Ile Glu Asp
81           200                 205                 210
83 ttt ggc gtg cac tgc aaa caa tat tat gcc tta gaa gtc tca tat ttc        780
84 Phe Gly Val His Cys Lys Gln Tyr Tyr Ala Leu Glu Val Ser Tyr Phe
85           215                 220                 225
87 aaa tca tct ttg gat cgt aaa cta ctt gag ctt ttg tgg aat aaa tac        828
88 Lys Ser Ser Leu Asp Arg Lys Leu Leu Glu Leu Leu Trp Asn Lys Tyr
89 230                 235                 240                 245
91 tgg gtg aat acc ctg agt tcc tct agc ttg ctt act aat gca gac tac        876
92 Trp Val Asn Thr Leu Ser Ser Ser Ser Leu Leu Thr Asn Ala Asp Tyr
93                 250                 255                 260
95 acc aca ggc cag gtg ttt gat ttg tct gag aag tta gag cag tcg gaa        924
96 Thr Thr Gly Gln Val Phe Asp Leu Ser Glu Lys Leu Glu Gln Ser Glu
97                 265                 270                 275
99 gcc caa ctg gga cgt ggc agt ttc atg ttg ggc tta gaa aca cat gac        972
100 Ala Gln Leu Gly Arg Gly Ser Phe Met Leu Gly Leu Glu Thr His Asp
101           280                 285                 290
103 cgc aag tcg gaa gac aaa ctt gcc aaa gct act aga gac agc tgt aaa        1020
104 Arg Lys Ser Glu Asp Lys Leu Ala Lys Ala Thr Arg Asp Ser Cys Lys
105           295                 300                 305
107 acc acc ata gaa gcc atc cat gga ctg atg tct cag gtt att aag gat        1068
108 Thr Thr Ile Glu Ala Ile His Gly Leu Met Ser Gln Val Ile Lys Asp
109 310                 315                 320                 325
111 aaa ctg ttt aat cag att aac gtt gct    tagtt accaccaagt acttctcaaa      1120
112 Lys Leu Phe Asn Gln Ile Asn Val Ala
113                 330
115 gctggtgtgt ggaaggaaaa gaagctcaag taacactttt aacccagtta ccaaaactca      1180
117 gattagaaga ctaaggtgct gtgtggtgtc ctgagtatta gcactgtaat aaaactatca      1240
119 cgtgaaaaaa aaaaaaaaaa aa                                               1262
122 <210> SEQ ID NO: 2
123 <211> LENGTH: 334
124 <212> TYPE: PRT
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125 <213> ORGANISM: Homo sapiens
127 <400> SEQUENCE: 2
128 Met Ala Ala Ser Gly Ser Gly Met Ala Gln Lys Thr Trp Glu Leu Ala
129  1               5                  10                  15
131 Asn Asn Met Gln Glu Ala Gln Ser Ile Asp Glu Ile Tyr Lys Tyr Asp
132              20                  25                  30
134 Lys Lys Gln Gln Gln Glu Ile Leu Ala Ala Lys Pro Trp Thr Lys Asp
135          35                  40                  45
137 His His Tyr Phe Lys Tyr Cys Lys Ile Ser Ala Leu Ala Leu Leu Lys
138          50                  55                  60
140 Met Val Met His Ala Arg Ser Gly Gly Asn Leu Glu Val Met Gly Leu
141  65                  70                  75                  80
143 Met Leu Gly Lys Val Asp Gly Glu Thr Met Ile Ile Met Asp Ser Phe
144                  85                  90                  95
146 Ala Leu Pro Val Glu Gly Thr Glu Thr Arg Val Asn Ala Gln Ala Ala
147              100                 105                 110
149 Ala Tyr Glu Tyr Met Ala Ala Tyr Ile Glu Asn Ala Lys Gln Val Gly
150          115                 120                 125
152 Arg Leu Glu Asn Ala Ile Gly Trp Tyr His Ser His Pro Gly Tyr Gly
153          130                 135                 140
155 Cys Trp Leu Ser Gly Ile Asp Val Ser Thr Gln Met Leu Asn Gln Gln
156 145                 150                 155                 160
158 Phe Gln Glu Pro Phe Val Ala Val Val Ile Asp Pro Thr Arg Thr Ile
159              165                 170                 175
161 Ser Ala Gly Lys Val Asn Leu Gly Ala Phe Arg Thr Tyr Pro Lys Gly
162              180                 185                 190
164 Tyr Lys Pro Pro Asp Glu Gly Pro Ser Glu Tyr Gln Thr Ile Pro Leu
165          195                 200                 205
167 Asn Lys Ile Glu Asp Phe Gly Val His Cys Lys Gln Tyr Tyr Ala Leu
168          210                 215                 220
170 Glu Val Ser Tyr Phe Lys Ser Ser Leu Asp Arg Lys Leu Leu Glu Leu
171 225                 230                 235                 240
173 Leu Trp Asn Lys Tyr Trp Val Asn Thr Leu Ser Ser Ser Ser Leu Leu
174              245                 250                 255
176 Thr Asn Ala Asp Tyr Thr Thr Gly Gln Val Phe Asp Leu Ser Glu Lys
177          260                 265                 270
179 Leu Glu Gln Ser Glu Ala Gln Leu Gly Arg Gly Ser Phe Met Leu Gly
180          275                 280                 285
182 Leu Glu Thr His Asp Arg Lys Ser Glu Asp Lys Leu Ala Lys Ala Thr
183          290                 295                 300
185 Arg Asp Ser Cys Lys Thr Thr Ile Glu Ala Ile His Gly Leu Met Ser
186 305                 310                 315                 320
188 Gln Val Ile Lys Asp Lys Leu Phe Asn Gln Ile Asn Val Ala
189              325                 330
192 <210> SEQ ID NO: 3
193 <211> LENGTH: 32
194 <212> TYPE: DNA
195 <213> ORGANISM: Artificial Sequence
197 <220> FEATURE:
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198 <223> OTHER INFORMATION: primer for WNV-Cp amplification
201 <400> SEQUENCE: 3
202 ccggaattct ctaaaaaacc aggtggcccc gg                              32
205 <210> SEQ ID NO: 4
206 <211> LENGTH: 33
207 <212> TYPE: DNA
208 <213> ORGANISM: Artificial Sequence
210 <220> FEATURE:
211 <223> OTHER INFORMATION: primer for WNV-Cp amplification
214 <400> SEQUENCE: 4
215 gactagcggt cgcacccgcg catcgagctc gcc                             33
218 <210> SEQ ID NO: 5
219 <211> LENGTH: 32
220 <212> TYPE: DNA
221 <213> ORGANISM: Artificial Sequence
223 <220> FEATURE:
224 <223> OTHER INFORMATION: primer for DNA sequencing
227 <400> SEQUENCE: 5
228 ctattcgatg atgaagatac cccaccaaac cc                              32
231 <210> SEQ ID NO: 6
232 <211> LENGTH: 33
233 <212> TYPE: DNA
234 <213> ORGANISM: Artificial Sequence
236 <220> FEATURE:
237 <223> OTHER INFORMATION: primer for DNA sequencing
240 <400> SEQUENCE: 6
241 tagcatctat gactttttgg ggcgttcaag tga                             33
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VERIFICATION SUMMARY DATE: 04/26/2005
PATENT APPLICATION: **US/10/531,543** TIME: 15:48:07

Input Set : **A:\PCT-KR2003-002190(Sequence List).txt**
Output Set: **N:\CRF4\04262005\J531543.raw**

L:5 M:270 C: Current Application Number differs, Replaced Current Application No
L:5 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:0 M:201 W: Mandatory field data missing, <130> FILE REFERENCE